

Comparison of MetAP2 Homologues (mouse = SEQ ID NO:13; rat = SEQ ID NO:17;  
human = SEQ ID NO:12; yeast = SEQ ID NO:14)

mouse	1	15	16	30	31	45	46	60	61	75	76	90
MAGVEQAASFGGHLN	GDLPDREEGTST	AEEAARRRRRRRRRR	KGAVSAVQQLDKES	GALVDEVAKQLESQA	LEEKERDDDDDDDDG							90
rat	MAGVEAASFGGHLN	RDLPDREEGTST	AEEAARRRRRRRRRR	KGAVSAVQQLDKES	GTSVDEVAKQLESQA	LEEKERDDDDDDDDG						90
human	MAGVEEVAASGSHLN	GDLPDREEGAAT	AEEAARRRRRRRRRR	KGPSAAGEQEPDKES	GASVDEVAKQLESQA	LEEKERDDDDDDDDG						90
yeast	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	38
mouse	91	105	106	120	121	135	136	150	151	165	166	180
DADGATGKKKKKKKK	KRGPVQTDPSVPI	CDLYPVGVPKQEC	EYPTQDGRTAAMRT	TSEKKALDQASEEI	WNDEREAFAHRQVR							180
rat	DGDGAAGKKKKKKKK	KRGPVQTDPSVPI	CDLYPVGVPKQEC	EYPTQDGRTAAMRT	TSEKKALDQASEEI	WNDEREAFAHRQVR						180
human	DGDGATGKKKKKKKK	KRGPVQTDPSVPI	CDLYPVGVPKQEC	EYPTQDGRTAAMRT	TSEKKALDQASEEI	WNDEREAFAHRQVR						180
yeast	ESKKKKKKKKKKKK	N-----	VKKI	ELLPDGKYPEGAM	DYHDFNLQRTTDEE	SRYLKRDLERA--EH	WNDVRKGAETIHRVR					116
mouse	181	195	196	210	211	225	226	240	241	255	256	270
KYVMSWIKPGMTMIE	ICEKLEDCSRKLKE	NGLNAG-----	LA	FPTGCSLNCCAHT	PNAGDTTVLQYDDIC	KIDFGTHISGRIDC						263
rat	KYVMSWIKPGMTMIE	ICEKLEDCSRKLKE	NGLNAG-----	LA	FPTGCSLNCCAHT	PNAGDTTVLQYDDIC	KIDFGTHISGRIDC					263
human	KYVMSWIKPGMTMIE	ICEKLEDCSRKLKE	NGLNAG-----	LA	FPTGCSLNCCAHT	PNAGDTTVLQYDDIC	KIDFGTHISGRIDC					263
yeast	RAIKDRIVPGMKLMD	IADMIENTTRKYTGA	ENLLAMEDPKSQSIG	FPTGLSLNHCAHFT	PNAGDKTVLKYEDEM	KVDYGVQVNGNIIDS						206
mouse	271	285	286	300	301	315	316	330	331	345	346	360
AFTVTENPKYDILIT	AVKDATNTGICAGI	DVRLCDVGEALQEV	ESYEVEIDGKTYQVK	PIRNLNGHSIGPYRI	HAGKTVPIVKGGEAT							353
rat	AFTVTENPKYDILIT	AVKDATNTGICAGI	DVRLCDVGEALQEV	ESYEVEIDGKTYQVK	PIRNLNGHSIGPYRI	HAGKTVPIVKGGEAT						353
human	AFTVTENPKYDILIT	AVKDATNTGICAGI	DVRLCDVGEALQEV	ESYEVEIDGKTYQVK	PIRNLNGHSIGPYRI	HAGKTVPIVKGGEAT						353
yeast	AFTVSFDQYDNLILA	AVKDATYTGIEKAGI	DVRLTDIGEALQEV	ESYEVEINGETTYQVK	PCRNLCGHSIAPYRI	HGKSVPIVKNGDTT						296
mouse	361	375	376	390	391	405	406	420	421	435	436	450
RMEEGEVAIETFGS	TGKGVHDDMECSHY	MKNFDVGHPVIRLPR	TKHLNVINENEGTL	AFCRRLDRLGESKY	LMALKNLCDLGI	IVDP						443
rat	RMEEGEVAIETFGS	TGKGVHDDMECSHY	MKNFDVGHPVIRLPR	TKHLNVINENEGTL	AFCRRLDRLGESKY	LMALKNLCDLGI	IVDP					443
human	RMEEGEVAIETFGS	TGKGVHDDMECSHY	MKNFDVGHPVIRLPR	TKHLNVINENEGTL	AFCRRLDRLGESKY	LMALKNLCDLGI	IVDP					443
yeast	KMEEGEHAETFGS	TGRGYVTAGGEVSHY	ARSAEDHQVMPITLDS	AKNLKTIIDRNEFTL	PFCRRYLDRLGQEKY	LFALNNLVHRHGLVQD						386
mouse	451	465	466	480								
YPPLCDIKGSYTAQF	EHTILLRPTCKEVVS	RGDDY--										478
rat	YPPLCDIKGSYTAQF	EHTILLRPTCKEVVS	RGDDY--									480
human	YPPLCDIKGSYTAQF	EHTILLRPTCKEVVS	RGDDY--									478
yeast	YPPLNDIPGSYTAQF	EHTILLHAHKEVVS	KGDDY--									421

Figure 1

Title: Dominant Negative Variants fo Mehtionine  
Aminopeptidase  
Inventor(s): Chang et al.  
Appln. No. 09/943,123  
Docket # 66153/45004

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## MetAP2

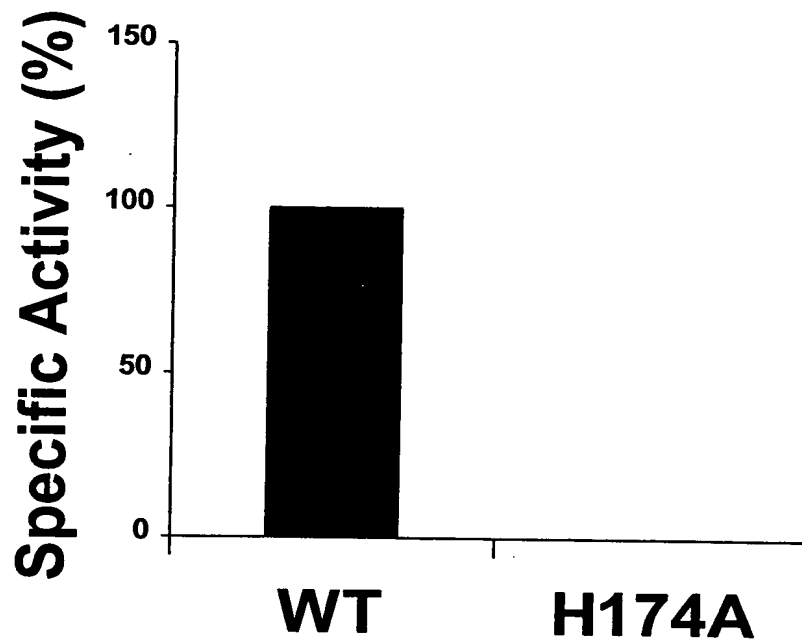
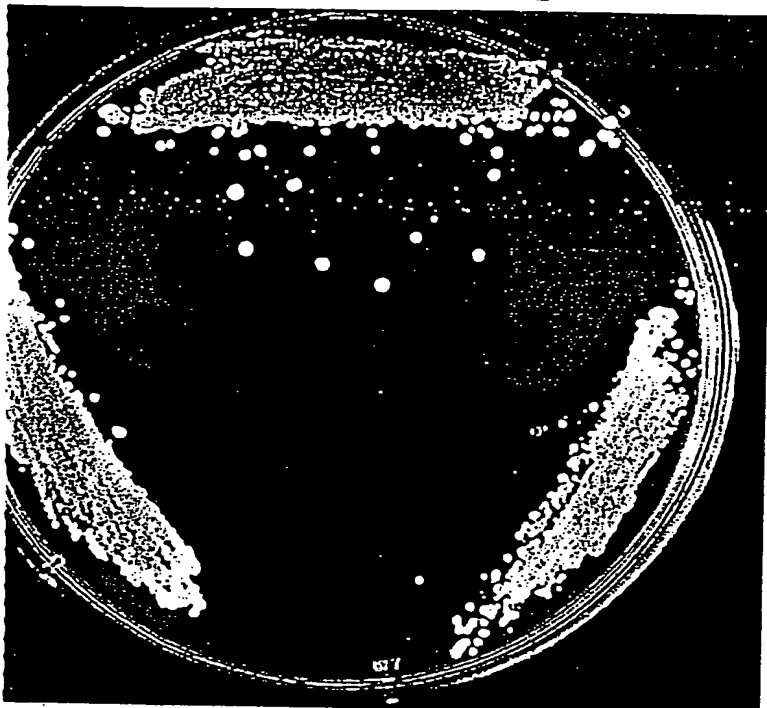
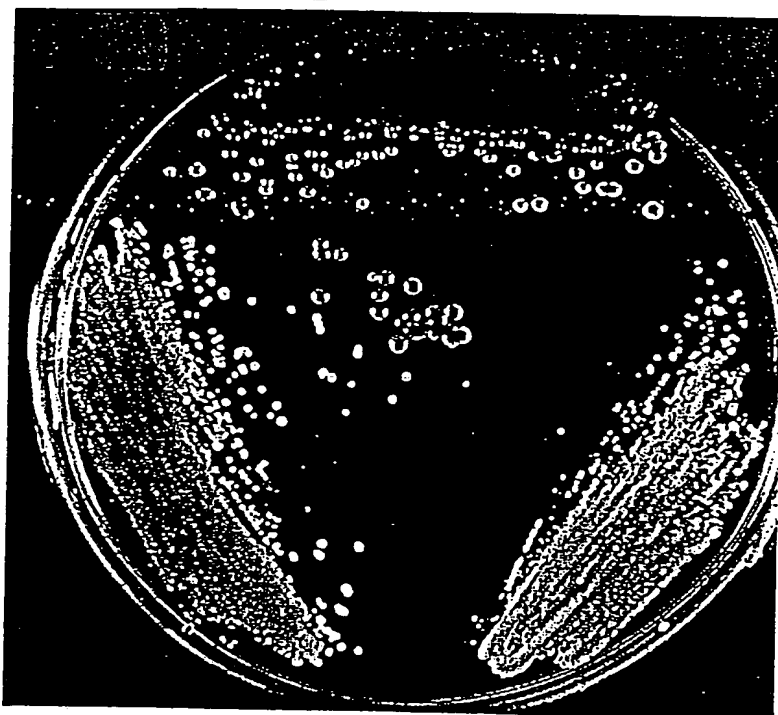


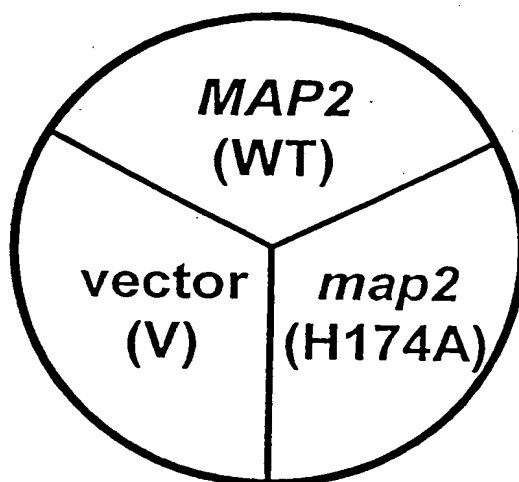
Figure 2



**A. Glucose**



**B. Galactose**



**FIGURE 3**

Title:	Dominant Negative Variants fo Mehtionine Aminopeptidase
Inventor(s):	Chang et al.
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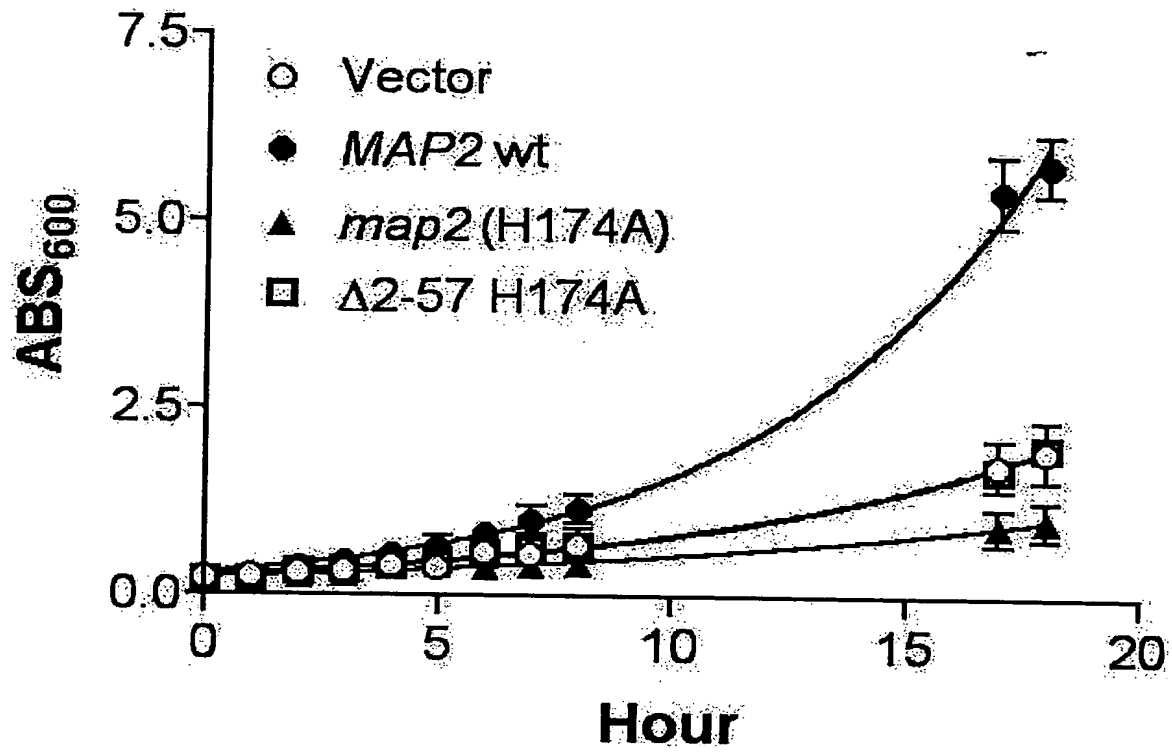
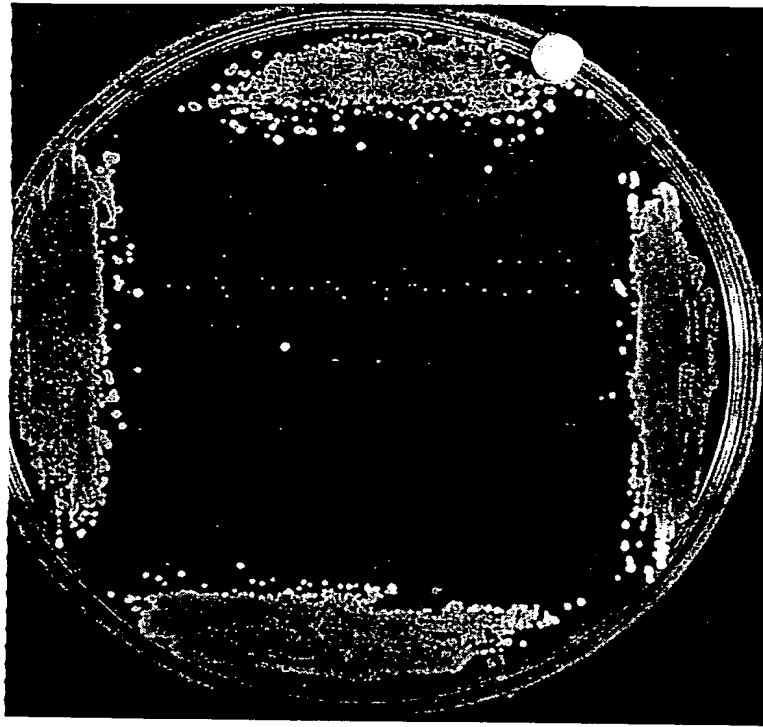
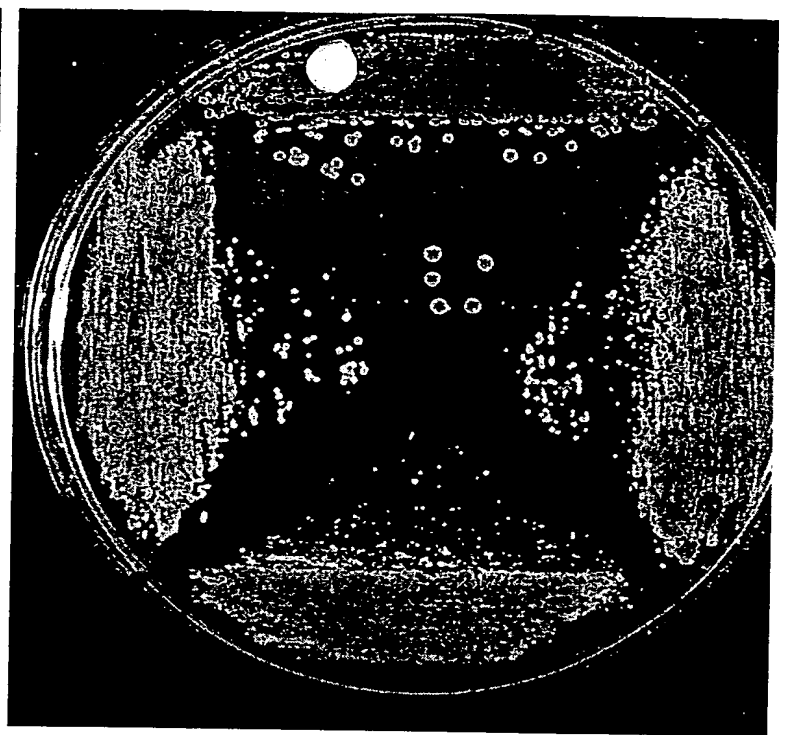


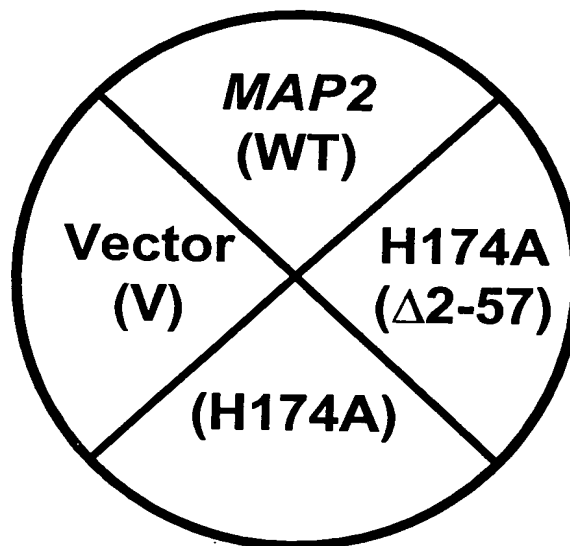
Figure 4



**A. Glucose**



**B. Galactose**



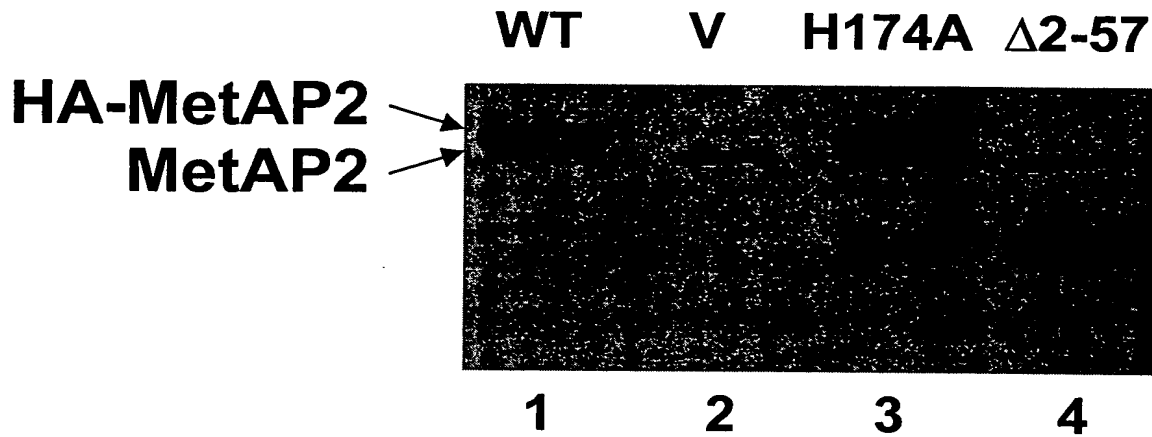
H174A-MetAP2 requires N-terminal residues 2-57 for inhibition of *map1Δ* growth under the GAL1 promoter.

**Figure 5**

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Inventor(s):	Chang et al.
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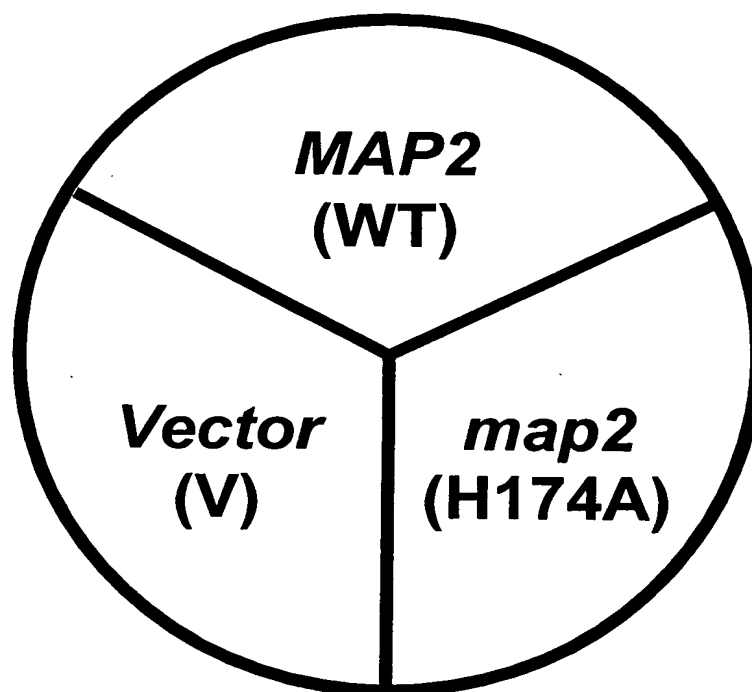
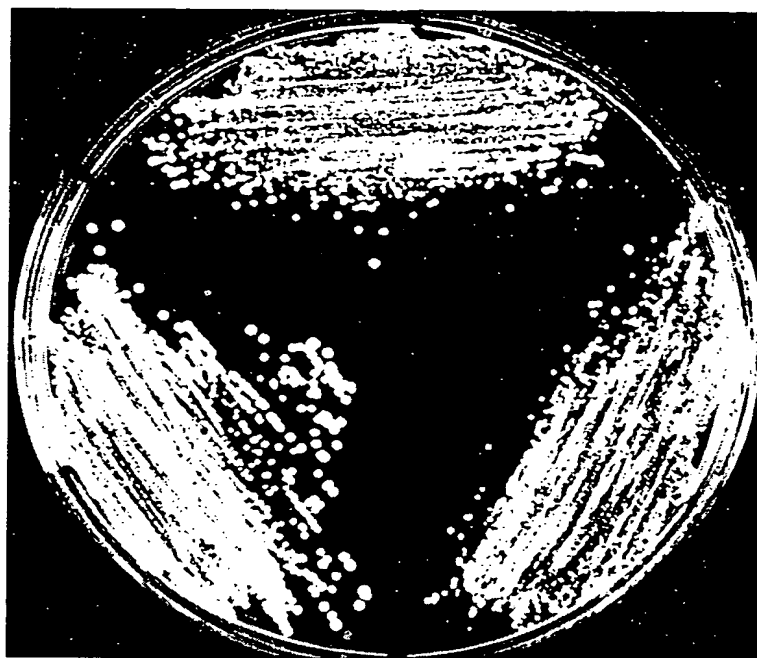
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Aminopeptidase  
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The steady state levels of each MetAP2 construct are comparable. Immunoblot comparison of HA-MetAP2 wt, HA-MetAP2 H174A, and MetAP2  $\Delta$ 2-57 H174A steady state levels in map1 $\Delta$ .

Figure 6



Overexpression of H174A-MetAP2 under the GPD promoter does not inhibit the growth of map2Δ

Figure 7

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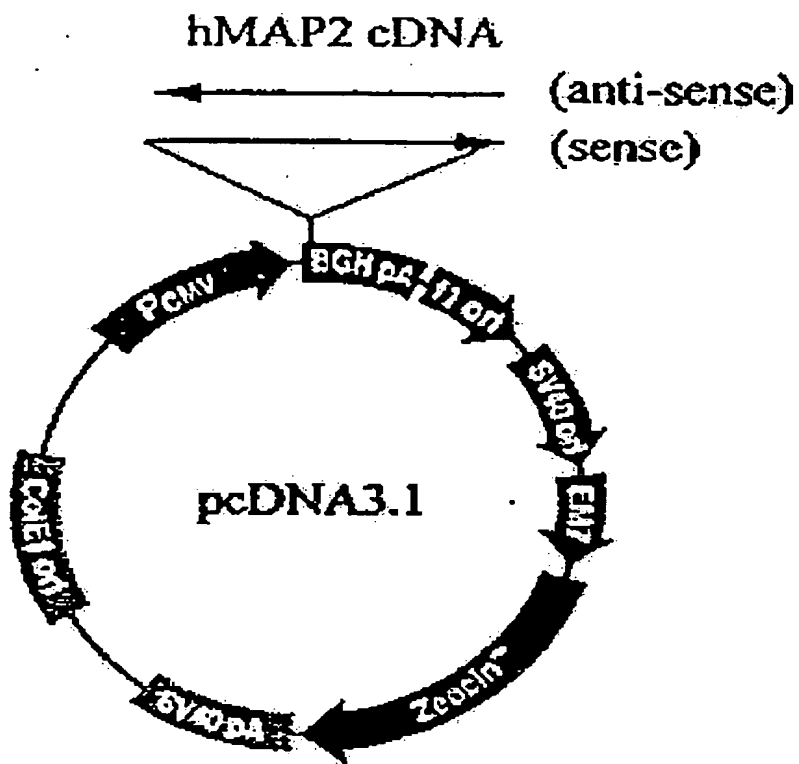


Figure 8



Title: Dominant Negative Variants fo Mehtionine  
Aminopeptidase

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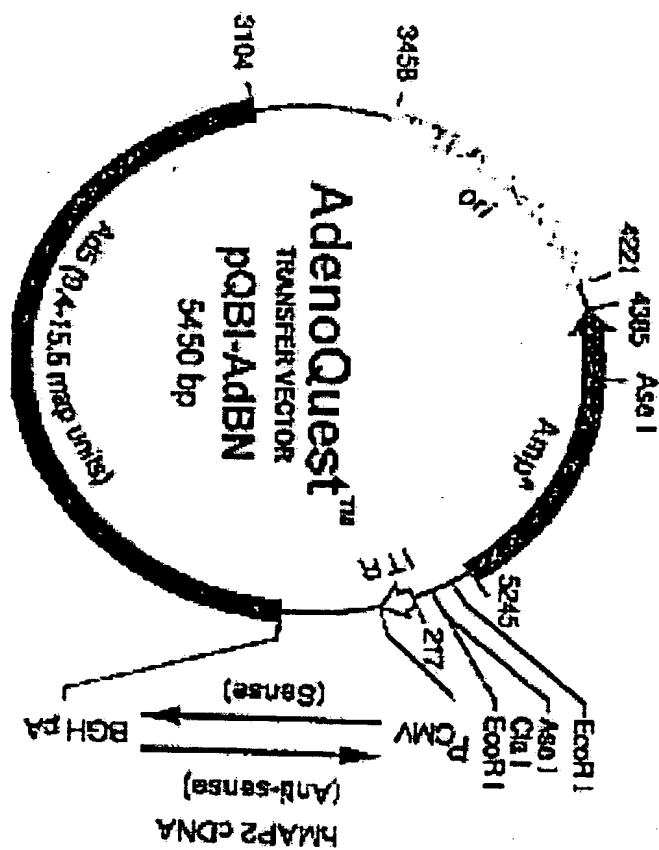


Figure 9

Title: Dominant Negative Variants fo Mehtionine  
Aminopeptidase  
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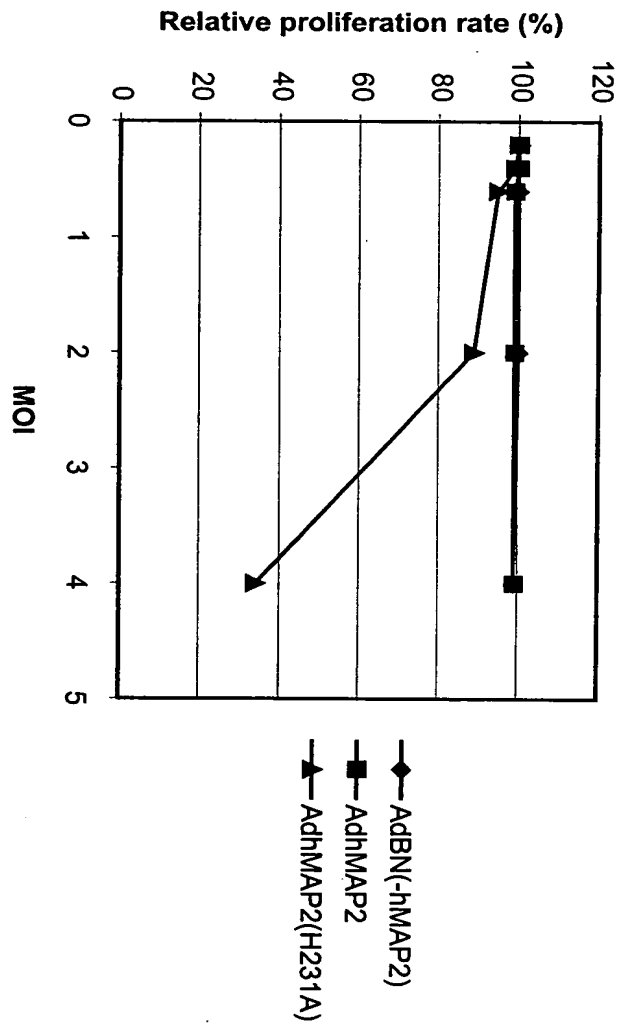


Figure 10

Title: Dominant Negative Variants fo Mehtionine  
 Aminoamidase  
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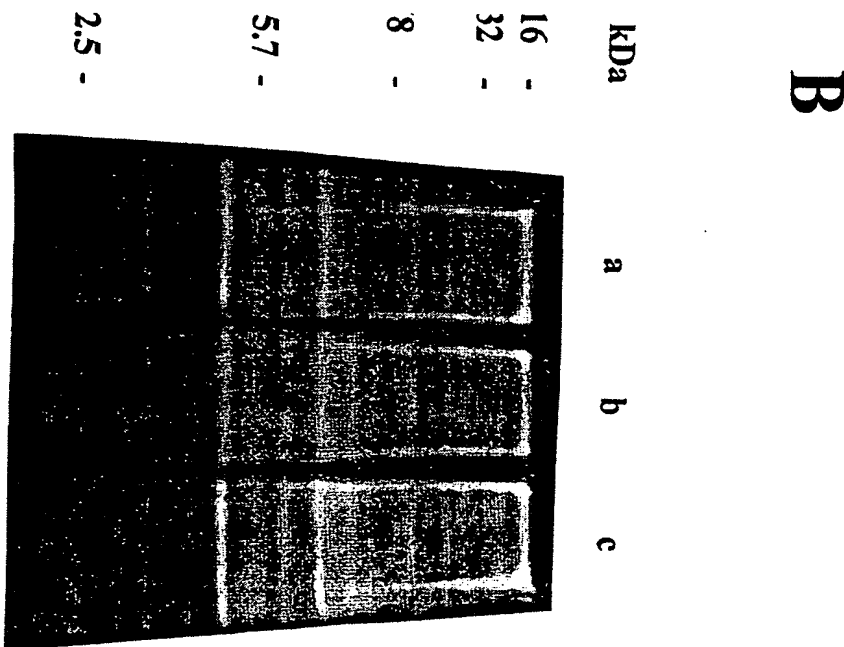
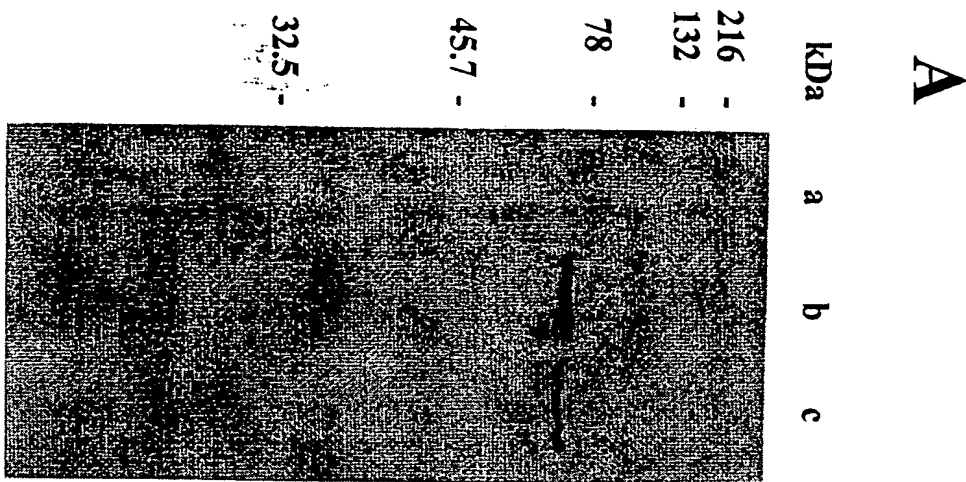


Figure 11